

MODELING PROTEIN FAMILIES AND HUMAN GENES: HIDDEN MARKOV MODELS AND A LITTLE BEYOND

Pierre Baldi

Jet Propulsion Laboratory
and
Division of Biology
California Institute of Technology

4800 Oak Grove Dr., M/S 303-310
Pasadena, CA 91109
Tel: (81 8)354-9038
FAX: (81 8)393-501 3
E-Mail: pfbaldi@juliet.caltech.edu

ABSTRACT

We will first give a brief overview of Hidden Markov Models (HMMS) and their use in Computational Molecular Biology. In particular, we will describe a detailed application of HMMs to the G-Protein-Coupled-Receptor Superfamily. We will also describe a number of analytical results on HMMS that can be used in discrimination tests, and data base mining. We will then discuss the limitations of HMMs and some new directions of research. If time permits, we will conclude with some recent results on the application of HMMs to human gene modeling and parsing.